

**Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of Claims:**

1-3 (cancelled).

4 (previously presented). A substantially pure polypeptide comprising the sequence identified as SEQ ID NO:1.

5 (previously presented). The polypeptide according to claim 4 with a molecular mass of about 20k.

6-21 (cancelled).

22 (previously presented). A pharmaceutical composition comprising the polypeptide of claim 50.

23-27 (cancelled).

28 (previously presented). A method for treating patients deficient in the activity of MASP-2 by administering to the patient the polypeptide of claim 50.

29-45 (cancelled).

46 (previously presented). A substantially pure polypeptide consisting of the sequence of SEQ ID NO:2, or of the sequence defined by position 16 to position 686 of SEQ ID NO:2.

47 (currently amended). A substantially pure polypeptide comprising an amino acid sequence at least 85% identical to the sequence defined by position 16 to position 686 of SEQ ID NO:2, wherein said polypeptide has at least one of the following activities

i) cleavage of C4 and activation of the complement in an in vitro assay for MBlectin complement pathway function; or

ii) serine protease activity; or

iii) mannan-binding lectin (MBL) associating activity

and where, if said amino acid sequence differs from the sequence defined by position 16 to position 686 of SEQ ID NO:2, it does

so solely by one or more substitutions selected from the group consisting of

Gly/Ala,

Val/Ile/Leu,

Asp/Glu,

Asn/Gln,

Ser/Thr,

Lys/Arg, and

Phe/Tyr.

48 (cancelled).

49 (previously presented). The polypeptide according to claim 47 in which the polypeptide comprises a sequence at least 90% identical to the sequence defined by position 16 to position 686 of SEQ ID NO:2.

50 (currently amended). A substantially pure polypeptide, which the polypeptide comprises an amino acid sequence at least 95% identical to the sequence defined by position 16 to position 686 of SEQ ID NO:2,

wherein said polypeptide has the following activities

- i) cleavage of C4 and activation of the complement in an in vitro assay for MBlectin complement pathway function; and
- ii) mannan-binding lectin (MBL) associating activity.

51 (currently amended). The polypeptide according to claim ~~47~~ 50, in which the polypeptide comprises a sequence at least 98% identical to the sequence defined by position 16 to position 686 of SEQ ID NO:2.

52 (currently amended). The polypeptide according to claim ~~47~~ 50, in which the polypeptide comprises a sequence at least 99% identical to the sequence defined by position 16 to position 686 of SEQ ID NO:2.

53 (cancelled).

54 (currently amended). The polypeptide according to claim 50 in which differences between the polypeptide sequence and SEQ ID NO:1 are limited to ~~conservative~~ substitutions selected from the group consisting of

Gly/Ala,

Val/Ile/Leu,

Asp/Glu,

Asn/Gln,

Ser/Thr,

Lys/Arg, and

Phe/Tyr.

55-56 (cancelled).

57 (previously presented). A substantially pure polypeptide comprising the amino acid sequence of position 16 to position 686 of SEQ ID NO:2.

58 (previously presented). The polypeptide of claim 4, consisting of the sequence of SEQ ID NO:1.

59 (previously presented). The polypeptide of claim 50 where said polypeptide is bound by a monoclonal antibody which binds mature MASP-2.

60 (previously presented). The polypeptide of claim 50 which comprises a contiguous 100 amino acid sequence which is completely identical to a sequence of 100 contiguous amino acids within the sequence from position 16 to position 686 of SEQ ID NO:2.

61 (previously presented). The polypeptide of claim 50 which comprises a sequence which, when aligned with SEQ ID NO:2, is identical to SEQ ID NO:2 at each position of SEQ ID NO:2 which is marked with an asterisk in Fig. 2 because it is a conserved residue position in MASP-2, MASP-1, Clr and Cls.

62 (previously presented). The polypeptide of claim 51 which

comprises a sequence which, when aligned with SEQ ID NO:2, is identical to SEQ ID NO:2 at each position of SEQ ID NO:2 which is marked with an asterisk in Fig. 2 because it is a conserved residue position in MASP-2, MASP-1, Clr and Cls.

63 (previously presented). The polypeptide of claim 52 which comprises a sequence which, when aligned with SEQ ID NO:2, is identical to SEQ ID NO:2 at each position of SEQ ID NO:2 which is marked with an asterisk in Fig. 2 because it is a conserved residue position in MASP-2, MASP-1, Clr and Cls.

64 (previously presented). The polypeptide of claim 54 which comprises a sequence which, when aligned with SEQ ID NO:2, is identical to SEQ ID NO:2 at each position of SEQ ID NO:2 which is marked with an asterisk in Fig. 2 because it is a conserved residue position in MASP-2, MASP-1, Clr and Cls.

65 (currently amended). The polypeptide according to claim 51 in which differences between the polypeptide sequence and SEQ ID NO:1 are limited to ~~conservative~~ substitutions selected from the group consisting of

Gly/Ala,

Val/Ile/Leu,

Asp/Glu,

Asn/Gln,

Ser/Thr,

Lys/Arg, and

Phe/Tyr.

66 (currently amended). The polypeptide according to claim 52 in which differences between the polypeptide sequence and SEQ ID NO:1 are limited to ~~conservative~~ substitutions selected from the group consisting of

Gly/Ala,

Val/Ile/Leu,

Asp/Glu,

Asn/Gln,

Ser/Thr,

Lys/Arg, and

Phe/Tyr.

67 (previously presented). The polypeptide of claim 65 which comprises a sequence which, when aligned with SEQ ID NO:2, is identical to SEQ ID NO:2 at each position of SEQ ID NO:2 which is marked with an asterisk in Fig. 2 because it is a conserved residue position in MASP-2, MASP-1, C1r and C1s.

68 (previously presented). The polypeptide of claim 66 which comprises a sequence which, when aligned with SEQ ID NO:2, is identical to SEQ ID NO:2 at each position of SEQ ID NO:2 which is marked with an asterisk in Fig. 2 because it is a conserved residue position in MASP-2, MASP-1, C1r and C1s.

69 (currently amended). The polypeptide of claim ~~53~~ 47 which comprises a sequence which, when aligned with SEQ ID NO:2, is identical to SEQ ID NO:2 at each position of SEQ ID NO:2 which is marked with an asterisk in Fig. 2 because it is a conserved residue position in MASP-2, MASP-1, C1r and C1s.

70-71 (cancelled).

72 (new). The polypeptide of claim 49 which comprises a sequence which, when aligned with SEQ ID NO:2, is identical to SEQ ID NO:2 at each position of SEQ ID NO:2 which is marked with an asterisk in Fig. 2 because it is a conserved residue position in MASP-2, MASP-1, C1r and C1s.